

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2002, 00:48:38 ; Search time 2351.15 Seconds

(without alignments)
175.416 Million cell updates/sec

Title: US-09-851-670-12

Perfect score: 25
Sequence: 1 acagctgcgcccatcaacatattc 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 586436

Minimum DB seq length: 0

Maximum DB seq length: 60

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pt:*
- 10: gb_ro:*
- 11: gb_sy:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_om:*
- 20: em_or:*
- 21: em_ov:*
- 22: em_pat:*
- 23: em_ph:*
- 24: em_pl:*
- 25: em_ro:*
- 26: em_sts:*
- 27: em_sy:*
- 28: em_un:*
- 29: em_vl:*
- 30: em_hlgo_hum:*
- 31: em_hlgo_inv:*
- 32: em_hlgo_rod:*
- 33: em_hlgo_hum:*
- 34: em_hlgo_inv:*
- 35: em_hlgo_rod:*
- 36: em_hlgo_other:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14.6	58.4	58	6	A48495	A48495 Sequence 16
2	14	56.0	50	6	AX097513	AX097513 Sequence 8
3	13.6	54.4	40	6	A84763	A84763 Sequence 8
4	13.6	54.4	57	6	A60847	A60847 Sequence 15
5	13.4	53.6	20	6	AX004424	AX004424 Sequence
6	13.4	53.6	29	6	AX137235	AX137235 Sequence
7	13.4	53.6	29	6	AX137236	AX137236 Sequence
8	13.4	53.6	36	6	A66390	A66390 Sequence 31
9	13.4	53.6	58	6	AX165076	AX165076 Sequence
10	13.4	53.6	58	6	A60214	A60214 Sequence 10
11	13.4	53.6	58	6	AR122290	AR122290 Sequence
12	13.2	52.8	34	6	AR092439	AR092439 Sequence
13	13.2	52.8	60	6	A29441	A29441 sequence ex
14	13	52.0	36	6	A66389	A66389 Sequence 31
15	13	52.0	50	10	AF071603	AF071603 Mus muscu
16	13	52.0	51	6	AX158449	AX158449 Sequence
17	12.8	51.2	48	6	IO4372	IO4372 Sequence 7
18	12.8	51.2	48	6	IO4381	IO4381 Sequence 16
19	12.8	51.2	51	6	AX165555	AX165555 Sequence
20	12.8	51.2	51	9	HS010893	HS010893 Homo sapi
21	12.6	50.4	32	6	AR082457	AR082457 Sequence
22	12.6	50.4	32	6	AR139013	AR139013 Sequence
23	12.6	50.4	38	6	AR047603	AR047603 Sequence
24	12.6	50.4	38	6	IS4655	IS4655 Sequence 23
25	12.6	50.4	50	6	AX097514	AX097514 Sequence
26	12.6	50.4	51	6	AX163122	AX163122 Sequence
27	12.4	49.6	21	6	AR051089	AR051089 Sequence
28	12.4	49.6	25	6	AX042678	AX042678 Sequence
29	12.4	49.6	25	6	AX043404	AX043404 Sequence
30	12.4	49.6	25	6	AX117676	AX117676 Sequence
31	12.4	49.6	30	6	AX035615	AX035615 Sequence
32	12.4	49.6	34	6	I81202	I81202 Sequence 7
33	12.4	49.6	36	6	AR031315	AR031315 Sequence
34	12.4	49.6	36	6	I84454	I84454 Sequence 2
35	12.4	49.6	40	6	I30556	I30556 Sequence 4
36	12.4	49.6	51	6	AX117677	AX117677 Sequence
37	12.4	49.6	54	6	AR083889	AR083889 Sequence
38	12.2	48.8	19	6	AX130042	AX130042 Sequence
39	12.2	48.8	21	6	AR138965	AR138965 Sequence
40	12.2	48.8	28	6	AR011468	AR011468 Sequence
41	12.2	48.8	28	6	AX188479	AX188479 Sequence
42	12.2	48.8	28	6	I18106	I18106 Sequence 34
43	12.2	48.8	37	6	AX039155	AX039155 Sequence
44	12.2	48.8	42	6	AR049554	AR049554 Sequence
45	12.2	48.8	42	6	AR049555	AR049555 Sequence

ALIGNMENTS

RESULT 1

LOCUS A48495 58 bp DNA PAT 07-MAR-1997

DEFINITION Sequence 16 from Patent WO9602654.

ACCESSION A48495

VERSION A48495.1 GI:2302273

KEYWORDS

SOURCE

ORGANISM

synthetic construct.

artificial sequence.

REFERENCE

1 (bases 1 to 58)

AUTHORS

JACOBS,E., SILVESTRE,N., MOUNGIN,B., BISSARDON,O. and JOLIVET,M.

TITLE

CONDIT TOXOPLASMA P30 EXPRESSION CASSETTE

JOURNAL

Patent: WO 9602654-A 16 01-FEB-1996;

TRANSGENE SA (FR)

Other publication FR 2722508 960119.

COMMENT

Location/Qualifiers

1..58

/organism="synthetic construct"

/gb_xref="taxon:32630"

BASE COUNT 17 a 21 c 13 g 7 t
ORIGIN

Query Match 58.4%; Score 14.6; DB 6; Length 58;
Best Local Similarity 81.0%; Pred. No. 1.3e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 acagctcgcccaataacat 21
||||| ||| ||| |||
Db 25 ACAGCTAGCCACATCACCAT 45

RESULT 2
AX097513/c 50 bp DNA PAT 30-MAR-2001
LOCUS AX097513
DEFINITION Sequence 32 from Patent WO0118217.
ACCESSION AX097513
VERSION AX097513.1 GI:13514145
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 50)
AUTHORS Peredelchouk, M., Vonstein, V. and Demlirjan, D.
TITLE Thermus promoters for gene expression
JOURNAL Patent: WO 0118217-A 32 15-MAR-2001;
Thermogen, Inc. (US)
FEATURES
Location/Qualifiers
source 1..50
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Putative promoter sequence"

BASE COUNT 16 a 11 c 8 g 15 t
ORIGIN

Query Match 56.0%; Score 14; DB 6; Length 50;
Best Local Similarity 77.3%; Pred. No. 2.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 aacgctggcccaatacata 22
||||| ||| ||| |||
Db 22 AAAGCTGCTCCTTAACAA 1

RESULT 3
A84763 40 bp DNA PAT 21-JAN-2000
LOCUS A84763
DEFINITION Sequence 8 from Patent WO9844135.
ACCESSION A84763
VERSION A84763.1 GI:6733631
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 40)
AUTHORS Hegemann, J. and Zimmermann, F.K.
TITLE METHOD FOR SCREENING ANTIMYCOTICALLY ACTIVE SUBSTANCES
JOURNAL Patent: WO 9844135-A 8 08-OCT-1998;
HEGEMANN JOHANNES (DE); ZIMMERMANN FRIEDRICH KARL (DE)
FEATURES
Location/Qualifiers
source 1..40
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 9 a 13 c 7 g 11 t
ORIGIN

Query Match 54.4%; Score 13.6; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 4e+04; 4; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 tcgcccccaataacatlc 25
|| ||| ||| ||| |||
Db 17 TCTACCCATGACATATTC 36

RESULT 4
A60847 57 bp DNA PAT 06-MAR-1998
LOCUS A60847
DEFINITION Sequence 156 from Patent WO9708320.
ACCESSION A60847
VERSION A60847.1 GI:3715468
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 57)
AUTHORS Knappik, A., Pack, P., Ilag, V., Ge, L., Moroney, S. and Plueckthun, A.
TITLE PROTEIN/(POLY)PEPTIDE LIBRARIES
JOURNAL Patent: WO 9708320-A 156 06-MAR-1997;
MORPHOSYS PROTEINOPTIMIERUNG (DE)
FEATURES
Location/Qualifiers
source 1..57
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 14 a 16 c 14 g 13 t
ORIGIN

Query Match 54.4%; Score 13.6; DB 6; Length 57;
Best Local Similarity 80.0%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ctgcgcccaataacatc 24
||||| ||| ||| |||
Db 17 CTCGCCACGATTAAAGATT 36

RESULT 5
AX004424 20 bp DNA PAT 24-AUG-2000
LOCUS AX004424
DEFINITION Sequence 6 from Patent WO9916899.
ACCESSION AX004424
VERSION AX004424.1 GI:9927883
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Anclil, J.L. and Cote, G.
TITLE Molecular diagnostic of glaucomas associated with chromosomes 2 and 6
JOURNAL Patent: WO 9916899-A 6 08-APR-1999;
ANCLIL JEAN LOUIS (CA); COTE GILLES (CA)
FEATURES
Location/Qualifiers
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="OLIGONUCLEOTIDE"

BASE COUNT 7 a 6 c 2 g 5 t
ORIGIN

Query Match 53.6%; Score 13.4; DB 6; Length 20;
Best Local Similarity 93.3%; Pred. No. 5.1e+04; 1; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 ccccaataacatc 24
||||| ||| ||| |||
Db 1 CCCCAATTAACAAT 15

RESULT 6

ORGANISM	unidentified
REFERENCE	1 (bases 1 to 36)
AUTHORS	Burg,S.H., Kast,W.M., Toes,R.E., Offringa,R., Melief,C. and Johannes,M.
TITLE	METHODS FOR SELECTING AND PRODUCING T CELL PEPTIDE EPITOPES AND VACCINES INCORPORATING SAID SELECTED EPITOPES
JOURNAL	Patent: WO 9741440-A 317 06-NOV-1997;
FEATURES	UNTY LEIDEN (NL)
source	Location/Qualifiers 1..36 /organism="unidentified" /db_xref="taxon:32644"
BASE COUNT	10 a 10 c 10 g 10 t
ORIGIN	
Query Match	53.6%; Score 13.4; DB 6; Length 36;
Best Local Similarity	73.9%; Pred. No. 5.1e+04;
Matches	17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY	2 cagctcgccccaataacataatt 24
Db	34 CCGCTAGAGCCCATTAACATAATT 12
RESULT	9
LOCUS	AX165076 50 bp DNA PAT 22-JUN-2001
DEFINITION	Sequence 271 from Patent WO0138586.
ACCESSION	AX165076
VERSION	AX165076.1 GI:14545905
KEYWORDS	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 50)
TITLE	Shinketsu,R.A. and Leach,M.
JOURNAL	Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
FEATURES	Patent: WO 0138586-A 271 31-MAY-2001;
source	Curagen Corporation (US)
misc-feature	Location/Qualifiers 1..50 /organism="Homo sapiens" /db_xref="taxon:9606"
variation	25..26 /note="Nucleotide deleted between bases 25 and 26 Accession number cg44030196"
BASE COUNT	11 a 17 c 7 g 15 t
ORIGIN	
Query Match	53.6%; Score 13.4; DB 6; Length 50;
Best Local Similarity	73.9%; Pred. No. 5.1e+04;
Matches	17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
OY	2 cagctcgccccaataacataatt 24
Db	17 CAGCTCAGCCCATTAAGACCAATT 39
RESULT	10
LOCUS	A60214 58 bp DNA PAT 06-MAR-1998
DEFINITION	Sequence 10 from Patent WO9708330.
ACCESSION	A60214
VERSION	A60214.1 GI:3715222
KEYWORDS	unidentified.
SOURCE	

ORGANISM unidentified
REFERENCE 1 (bases 1 to 58)
AUTHORS Collins, M.K., Weiss, R.A., Takeuchi, Y. and Cosset, F.
TITLE EXPRESSION SYSTEMS
JOURNAL Patent: WO 9708330-A 10 06-MAR-1997;
CANCER RES CAMPAIGN TECH (GB)
FEATURES
source 1. 58
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 15 a 19 c 12 g 12 t
ORIGIN

Query Match 53.6%; Score 13.4; DB 6; Length 58;
Best Local Similarity 73.9%; Pred. No. 5.1e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 cagctcgccccaataacatact 24
||||| ||| ||| ||| ||| |||
Db 25 CAGCGCGCCACATGAACACTT 47

RESULT 11
AR122290 58 bp DNA PAT 16-MAY-2001
LOCUS AR122290
DEFINITION Sequence 10 from patent US 6165715.
ACCESSION AR122290
VERSION AR122290.1 GI:14106607
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 58)
AUTHORS Collins, M., KatherineLeVing, Weiss, R., Anthony, Takeuchi, Y. and Cosset, F.
TITLE Expression systems
JOURNAL Patent: US 6165715-A 10 26-DEC-2000;
FEATURES Location/Qualifiers
source 1. 58
/organism="unknown"
BASE COUNT 15 a 19 c 12 g 12 t
ORIGIN

Query Match 53.6%; Score 13.4; DB 6; Length 58;
Best Local Similarity 73.9%; Pred. No. 5.1e+04;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 cagctcgccccaataacatact 24
||||| ||| ||| ||| ||| |||
Db 25 CAGCGCGCCACATGAACACTT 47

RESULT 12
AR092439 34 bp DNA PAT 08-SEP-2000
LOCUS AR092439
DEFINITION Sequence 21 from patent US 5998164.
ACCESSION AR092439
VERSION AR092439.1 GI:10019193
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 34)
AUTHORS Li, Y., Cao, L., Ni, J., Gentz, R., Bult, C.J., Sutton, G.G. III and Rosen, C.A.
TITLE Polynucleotides encoding human G-protein coupled receptor GPR2
JOURNAL Patent: US 5998164-A 21 07-DEC-1999;
FEATURES Location/Qualifiers
source 1. 34
/organism="unknown"

BASE COUNT 11 a 11 c 6 g 6 t
ORIGIN

Query Match 52.8%; Score 13.2; DB 6; Length 34;
Best Local Similarity 83.3%; Pred. No. 6.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 agctcgccccaataacata 20
||||| ||| ||| ||| |||
Db 6 AGCTTGCCACCATGACACA 23

RESULT 13
A29441 60 bp DNA PAT 22-AUG-1996
LOCUS A29441
DEFINITION sequence expressed in pre-B cells.
ACCESSION A29441
VERSION A29441.1 GI:1831980
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 60)
AUTHORS Bauer, S.R., Kudo, A., Melchers, G.F. and Sakaguchi, N.
TITLE Nucleotide sequences which are selectively expressed in pre-B cells
JOURNAL Patent: EP 0269127-A 59 01-JUN-1988;
F. HOFFMANN-LA ROCHE AG
FEATURES Location/Qualifiers
source 1. 60
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 10 a 21 c 13 g 16 t
ORIGIN

Query Match 52.8%; Score 13.2; DB 6; Length 60;
Best Local Similarity 83.3%; Pred. No. 6.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 gccccaataacatact 25
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Db 34 GCCACCATGACATCTTC 51

RESULT 14
A66389 36 bp DNA PAT 29-MAR-1999
LOCUS A66389
DEFINITION Sequence 316 from patent WO9741440.
ACCESSION A66389
VERSION A66389.1 GI:4538076
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 36)
AUTHORS Burg, S.H., Kast, W.M., Toes, R.E., Offringa, R., Melief, C. and Johannes, M.
TITLE METHODS FOR SELECTING AND PRODUCING T CELL PEPTIDE EPITOPES AND VACCINES INCORPORATING SAID SELECTED EPITOPES
JOURNAL Patent: WO 9741440-A 316 06-NOV-1997;
UNIV LEIDEN (NL)
FEATURES Location/Qualifiers
source 1. 36
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 9 a 9 c 7 g 11 t
ORIGIN

Query Match 52.0%; Score 13; DB 6; Length 36;
Best Local Similarity 76.2%; Pred. No. 8.1e+04;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 gctgcgccattacatatt 24
 ||| | ||||| |||||
 Db 1 GCTAGAGCCATTACATATT 21

RESULT 15
 AF071603/c

LOCUS AF071603 50 bp DNA ROD 26-JAN-1999
 DEFINITION Mus musculus clone CPJ-11 immunoglobulin heavy chain D-J region
 (VHJ558-D-J) gene, partial sequence.

ACCESSION AF071603
 VERSION AF071603.1 GI:3290190

KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Klonowski, K.D., Primiano, L.L. and Monestier, M.
 TITLE Atypical VH-D-JH rearrangements in newborn autoimmune MRI mice
 JOURNAL J. Immunol. 162 (3), 1566-1572 (1999)
 MEDLINE 99138837

REFERENCE
 AUTHORS Monestier, M. and Klonowski, K.
 TITLE Direct Submission
 JOURNAL Submitted (12-JUN-1998) Microbiology and Immunology, Temple
 University School of Medicine, 3400 N. Broad St., Philadelphia, PA
 19140, USA

FEATURES
 source Location/Qualifiers
 1..50

/organism="Mus musculus"
 /strain="C3H +/+"
 /db_xref="taxon:10090"
 /tissue_type="liver"
 /dev_stage="newborn"
 /rearranged
 /clone="CPJ-11"
 <1..>50
 /gene="VHJ558-D-J"
 /note="possible frameshift at D-J junction during
 rearrangement may result in nonfunctional immunoglobulin
 heavy chain"

gene

BASE COUNT 11 a 11 c 16 g 12 t
 ORIGIN

Query Match 52.0%; Score 13; DB 10; Length 50;
 Best Local Similarity 76.2%; Pred. No. 8.1e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0;

QY 5 ctcgcccattacatattc 25
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 Db 33 CTTGCCCCGTAACCTAGTC 13

Search completed: March 9, 2002, 00:48:39
 Job time: 11120 sec

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